09/897,069

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=> d his

     (FILE 'HOME' ENTERED AT 18:29:31 ON 24 MAR 2004)

     FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 18:29:44 ON 24 MAR
     2004
L1        20381 S C(W)ELEGANS
L2        26952 S SENSITIVE(5A)(DRUG OR AGENT OR CHEMICALS)
L3            0 S L1(7A)L2
L4           18 S L1 AND L2
L5          434 S L1 AND PARASITE
L6            0 S L5 AND L2
L7            5 DUP REM L4 (13 DUPLICATES REMOVED)

=> d bib ab 1-5 l7

L7   ANSWER 1 OF 5     MEDLINE on STN                    DUPLICATE 1
AN   2003411794     MEDLINE
DN   PubMed ID: 12951420
TI   Effects of 17beta-estradiol, bisphenol A and tributyltin chloride on germ
     cells of Caenorhabditis elegans.
AU   Hoshi Hidenobu; Kamata Yoichi; Uemura Takashi
CS   Graduate School of Agriculture and Biological Sciences, Osaka Prefecture
     University, Gakuen-cho, Sakai, Osaka, Japan.
SO   Journal of veterinary medical science / the Japanese Society of Veterinary
     Science, (2003 Aug) 65 (8) 881-5.
     Journal code: 9105360. ISSN: 0916-7250.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200312
ED   Entered STN: 20030903
     Last Updated on STN: 20031218
     Entered Medline: 20031205
AB   Effects of a one-generation exposure to a natural estrogen,
     17beta-estradiol (E2), and environmental pollutants such as bisphenol A
     (BPA) and tributyltin chloride (TBTCL) on the number of germ cells were
     investigated in the hermaphrodite Caenorhabditis elegans. The eggs of
     gravid adult worms isolated by alkaline hypochlorite treatment were seeded
     on a test chemical-containing NGM (nematode growth medium) agar plate
     without cholesterol. After incubation for 6 days at 16 degrees C, the
     germ cells of adult worms were stained with 4', 6-diamino-2-phenylindole
     dihydrochloride (DAPI). The staining procedure was completed within one
     hour and the stained germ cells were counted under a fluorescence
     microscope without dissection. The number of germ cells in the worms
     treated with E2 (10(-10)-10(-6) M) and BPA (10(-9)-10 (-5) M) was
     significantly increased. Maximal increases were observed at 10(-8) M E2
     (156 +/- 15.3% of control) and 10(-5) M BPA (168 +/- 20.0 % of control).
     TBTCL (10(-9)-10(-6) M) significantly decreased the number of germ cells.
     The minimal decrease was observed at 10(-6) M TBTCL (30.2 +/- 3.51% of
     control). These results indicate that changes in the number of germ cells
     are a sensitive indicator of the effects of chemicals
     on the reproductive system. Since the method described in this paper is a
     novel, simple, time- and money-saving bioassay, C.
     elegans is an excellent model with which to determine the
     reproductive toxicity of chemicals including environmental pollutants.

L7   ANSWER 2 OF 5     MEDLINE on STN                    DUPLICATE 2
AN   2002387336     MEDLINE
DN   PubMed ID: 12135927
TI   The C. elegans POU-domain transcription factor UNC-86
     regulates the tph-1 tryptophan hydroxylase gene and neurite outgrowth in
```

specific serotonergic neurons.
AU Sze Ji Ying; Zhang Shenyuan; Li Jie; Ruvkun Gary
CS Department of Anatomy and Neurobiology, College of Medicine, University of California, Irvine, Irvine, CA 92697, USA.. jsze@uci.edu
SO Development (Cambridge, England), (2002 Aug) 129 (16) 3901-11.
Journal code: 8701744. ISSN: 0950-1991.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200209
ED Entered STN: 20020724
Last Updated on STN: 20020912
Entered Medline: 20020911
AB A fundamental question in developmental neurobiology is how a common neurotransmitter is specified in different neuronal types?. We describe cell-specific regulation of the serotonergic phenotype by the **C. elegans** POU-transcription factor UNC-86. We show that unc-86 regulates particular aspects of the terminal neuronal identity in four classes of serotonergic neurons, but that the development of the ADF serotonergic neurons is regulated by an UNC-86-independent program. In the NSM neurons, the role of unc-86 is confined in late differentiation; the neurons are generated but do not express genes necessary for serotonergic neurotransmission. unc-86-null mutations affect the expression in NSM of tph-1, which encodes the serotonin synthetic enzyme tryptophan hydroxylase, and cat-1, which encodes a vesicular transporter that loads serotonin into synaptic vesicles, suggesting that unc-86 coordinately regulates serotonin synthesis and packaging. However, unc-86-null mutations do not impair the ability of NSM to reuptake serotonin released from the ADF serotonergic chemosensory neurons and this serotonin reuptake is **sensitive** to the serotonin reuptake block **drugs** imipramine and fluoxetine, demonstrating that serotonin synthesis and reuptake is regulated by distinct factors. The NSM neurons in unc-86-null mutants also display abnormal neurite outgrowth, suggesting a role of unc-86 in regulating this process as well.

L7 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 3
AN 96355334 MEDLINE
DN PubMed ID: 8702744
TI Identification of a Drosophila melanogaster glutamate-gated chloride channel **sensitive** to the antiparasitic **agent** avermectin.
AU Cully D F; Paress P S; Liu K K; Schaeffer J M; Arena J P
CS Department of Genetics and Molecular Biology, Merck Research Laboratories, Rahway, New Jersey 07065-0900, USA.
SO Journal of biological chemistry, (1996 Aug 16) 271 (33) 20187-91.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U58776
EM 199610
ED Entered STN: 19961015
Last Updated on STN: 19970203
Entered Medline: 19961003
AB Glutamate-gated chloride channels, members of the ligand-gated ion channel superfamily, have been shown in nematodes and in insects to be a target of the antiparasitic agent avermectin. Two subunits of the Caenorhabditis elegans glutamate-gated chloride channel have been cloned: GluCl-alpha and GluCl-beta. We report the cloning of a Drosophila melanogaster glutamate-gated chloride channel, DrosGluCl-alpha, which shares 48% amino acid and 60% nucleotide identity with the **C. elegans** GluCl channels. Expression of DrosGluCl-alpha in Xenopus oocytes produces

a homomeric chloride channel that is gated by both glutamate and avermectin. The DrosGluCl-alpha channel has several unique characteristics not observed in **C. elegans** GluCl: dual gating by avermectin and glutamate, a rapidly desensitizing glutamate response, and a lack of potentiation of the glutamate response by avermectin. The pharmacological data support the hypothesis that the DrosGluCl-alpha channel represents the arthropod H-receptor and an important target for the avermectin class of insecticides.

L7 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 4
AN 89313989 MEDLINE
DN PubMed ID: 2747711
TI Rad-2-dependent repair of radiation-induced chromosomal aberrations in Caenorhabditis elegans.
AU Sadaie T; Sadaie Y
CS Radioisotope Center, National Institute of Genetics, Japan.
NC 1-AG-9-2113 (NIA)
SO Mutation research, (1989 Jul) 218 (1) 25-31.
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198908
ED Entered STN: 19900309
Last Updated on STN: 19970203
Entered Medline: 19890823
AB A method involving light microscopy was developed and utilized for the observation of gamma- or ultraviolet-induced aberrations of the chromosomes of Caenorhabditis elegans var. Bristol (N2). Gravid worms were irradiated and the chromosomes were examined in the early embryos derived from eggs fertilized after the irradiation. The frequency of gamma-induced aberrations in the early embryonic cells of **C. elegans** increased proportionally with the dosage of gamma-rays. It decreased greatly following incubation of the irradiated gravid worms for 2 days. This decrease was blocked by the rad-2 mutation but not by the rad-1 mutation of the same epistasis group. Both mutations make worms **sensitive** to radiation and **chemicals**. In addition, the hatchability of eggs laid by the rad-2 mutant after irradiation was restored very quickly as was that of the wild-type strain. Ultraviolet irradiation, on the other hand, induced few aberrations in both the wild-type and rad-1 strains, but it caused an elevated frequency of aberrations in the rad-2 strain. Ultraviolet irradiation strongly blocked the separation of chromosomes of the rad-2 strain. Furthermore, hatchability was very low in eggs laid by ultraviolet-irradiated rad-2 worms. These results suggest the existence of a rad-2-dependent mechanism for gonadal repair of chromosomal aberrations, including chromosomal non-separation, and indicate that gamma-induced chromosome aberrations are not fatal to the hatching of Caenorhabditis elegans which has holocentric chromosomes.

L7 ANSWER 5 OF 5 MEDLINE on STN DUPLICATE 5
AN 84032491 MEDLINE
DN PubMed ID: 6630208
TI RNA polymerase II from wild type and alpha-amanitin-resistant strains of Caenorhabditis elegans.
AU Sanford T; Golomb M; Riddle D L
NC HD00367 (NICHD)
HD11239 (NICHD)
NO1 AG 9 2113 (NIA)
SO Journal of biological chemistry, (1983 Nov 10) 258 (21) 12804-9.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)

LA English
FS Priority Journals
EM 198312
ED Entered STN: 19900319
Last Updated on STN: 19970203
Entered Medline: 19831217

AB DNA-dependent RNA polymerases I, II, and III have been isolated from the soil nematode, Caenorhabditis elegans, and RNA polymerase II has been partially purified. The sensitivities of these enzymes to alpha-amanitin resemble those of the cognate enzymes from vertebrates. RNA polymerase II from **C. elegans** is 50% inhibited by 7 ng/ml of the amatoxin and RNA polymerase III by 80 micrograms/ml, whereas RNA polymerase I is insensitive to 500 micrograms/ml. We have obtained mutants of **C. elegans** which can grow and reproduce in concentrations of alpha-amanitin which arrest development of wild type animals. One of these mutants (DR432) has an altered RNA polymerase II which in partially purified extracts is 150 times less **sensitive** to the **drug** than the wild type enzyme. The mutation, ama-1(m130), in DR432 is dominant and maps near dpy-13 on linkage group IV. RNA polymerase II isolated from ama-1/+ heterozygotes contains equal proportions of two components, corresponding in alpha-amanitin sensitivity to the enzymes from DR432 and wild type. Thus, ama-1 appears to affect a subunit of RNA polymerase II.

=> d bib ab 1-19 l9

L9 ANSWER 1 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:30537 BIOSIS
DN PREV200300030537
TI Genetic approaches to programmed cell death: Achievements and questions. Original Title: Approches genetiques de la mort cellulaire programmee: Succes et questions..
AU Adam, Myriam; Levraud, Jean-Pierre; Golstein, Pierre [Reprint Author]
CS Centre d'Immunologie de Marseille-Luminy, Cnrs-Inserm, Universite Mediterranee, Parc Scientifique de Luminy, Case 906, 13288, Marseille Cedex, 9, France
golstein@ciml.univ-mrs.fr
SO M-S (Medecine Sciences), (Aout-Septembre 2002) Vol. 18, No. 8-9, pp. 831-840. print.
ISSN: 0767-0974.
DT Article
General Review; (Literature Review)
LA French
ED Entered STN: 8 Jan 2003
Last Updated on STN: 8 Jan 2003
AB A useful approach to study molecular mechanisms of cell death is, classically, mutagenesis followed with identification of the altered gene. For caspase-dependent cell death, this has provided spectacular results in the nematode C. elegans more than in other organisms. Often different molecules have been identified as a function of the investigated organism. These differences reflect, sometimes the existence of pathways seemingly unique to certain species, sometimes selection biases linked to peculiarities of the organisms under investigation.

L9 ANSWER 2 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:466663 BIOSIS
DN PREV200200466663
TI What does a worm want with 20,000 genes? The evolution of plant-parasitism, and the essential-gene conundrum.
AU Bird, D. [Reprint author]; Scholl, E. S.
CS Center for the Biology of Nematode Parasitism, North Carolina State University, Raleigh, NC, 27695, USA
SO Phytopathology, (June, 2002) Vol. 92, No. 6 Supplement, pp. S103. print.
Meeting Info.: 2002 Annual Meeting of the American Phytopathological Society. Milwaukee, WI, USA. July 27-31, 2002.
CODEN: PHYTAJ. ISSN: 0031-949X.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 4 Sep 2002
Last Updated on STN: 4 Sep 2002
AB The fully-sequenced genome of bacterivorous nematode C. elegans encodes 20,000 protein and RNA genes. The largest gene family (approximately 1,000 members) encodes G-protein-coupled receptors, many of which are olfactory receptor, indicative of the sophistication with which nematodes interact with the environment. Unlike lab-reared C. elegans for which many of the genes are dispensable, behavioral and other aspects of their lifestyle render many of these non-essential genes as being essential in parasites. EST-sequencing projects have revealed many orthologs of **C. elegans** genes in plant-**parasites**, including some apparently nematode-specific sequences. Some genes expressed by plant **parasites** are absent from **C. elegans**, including a cadre of genes apparently acquired from microbes. We are endeavoring to experimentally validate our computational predictions of horizontal gene-transfer, and speculate that such events played crucial roles in speciation of plant-parasitic nematodes.

L9 ANSWER 3 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2002:587424 BIOSIS
DN PREV200200587424
TI RNA interference of peroxisome-related genes in C. elegans: A new model for human peroxisomal disorders.
AU Petriv, Oleh I.; Pilgrim, David B.; Rachubinski, Richard A. [Reprint author]; Titorenko, Vladimir I.
CS Dept. of Cell Biology, Univ. of Alberta, Medical Sciences Bldg. 5-14, Edmonton, AB, T6G 2H7, Canada
rick.rachubinski@ualberta.ca
SO Physiological Genomics, (October, 2002) Vol. 10, pp. 79-91. print.
ISSN: 1094-8341.
DT Article
LA English
ED Entered STN: 13 Nov 2002
Last Updated on STN: 13 Nov 2002
AB RNA-mediated interference (RNAi) for the posttran-scriptional silencing of genes was used to evaluate the importance of various peroxisomal enzymes and peroxins for the development of Caenorhabditis elegans and to compare the roles of these proteins in the nematode to their roles in yeasts and humans. The nematode counterparts of the human ATP-binding cassette half-transporters, the enzymes alkyldihydroxyacetonephosphate synthase and DELTA3,5-DELTA2,4-dienoyl-CoA isomerase, the receptors for peroxisomal membrane and matrix proteins (Pex19p and Pex5p), and components of the docking and translocation machineries for matrix proteins (Pex13p and Pex12p) are essential for the development of C. elegans. Unexpectedly, RNAi silencing of the acyl-CoA synthetase-mediated activation of fatty acids, the alpha- and beta-oxidation of fatty acids, the intraperoxisomal decomposition of hydrogen peroxide, and the peroxins Pex1p, Pex2p, and Pex6p had no apparent effect on C. elegans development. The described analysis of functional gene knockouts through RNAi provides a basis for the use of C. elegans as a valuable model system with which to study the molecular and physiological defects underlying the human peroxisomal disorders.

L9 ANSWER 4 OF 19 MEDLINE on STN
AN 2002620069 MEDLINE
DN PubMed ID: 12372145
TI Conservation of long-range synteny and microsynteny between the genomes of two distantly related nematodes.
AU Guiliano D B; Hall N; Jones S J M; Clark L N; Corton C H; Barrell B G; Blaxter M L
CS Institute of Cell, Animal and Population Biology, University of Edinburgh, Edinburgh EH9 3JT, UK.
SO Genome biology, (2002 Sep 26) 3 (10) RESEARCH0057.
Journal code: 100960660. ISSN: 1465-6914.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AL606837
EM 200212
ED Entered STN: 20021017
Last Updated on STN: 20030105
Entered Medline: 20021220
AB BACKGROUND: Comparisons between the genomes of the closely related nematodes Caenorhabditis elegans and Caenorhabditis briggsae reveal high rates of rearrangement, with a bias towards within-chromosome events. To assess whether this pattern is true of nematodes in general, we have used genome sequence to compare two nematode species that last shared a common ancestor approximately 300 million years ago: the model **C. elegans** and the filarial **parasite** Brugia malayi.
RESULTS: An 83 kb region flanking the gene for Bm-mif-1 (macrophage migration inhibitory factor, a B. malayi homolog of a human cytokine) was sequenced. When compared to the complete genome of C. elegans, evidence

for conservation of long-range synteny and microsynteny was found. Potential C. elegans orthologs for II of the 12 protein-coding genes predicted in the B. malayi sequence were identified. Ten of these orthologs were located on chromosome I, with eight clustered in a 2.3 Mb region. While several, relatively local, intrachromosomal rearrangements have occurred, the order, composition, and configuration of two gene clusters, each containing three genes, was conserved. Comparison of B. malayi BAC-end genome survey sequence to C. elegans also revealed a bias towards intrachromosome rearrangements. CONCLUSIONS: We suggest that intrachromosomal rearrangement is a major force driving chromosomal organization in nematodes, but is constrained by the interdigitation of functional elements of neighboring genes.

L9 ANSWER 5 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:423188 BIOSIS
DN PREV200200423188
TI Natural variation in the response of **C. elegans** towards **parasite** attack.
AU Schulenburg, H. [Reprint author]
CS Institute of Animal Evolution and Ecology, Westphalian Wilhelms-University Muenster, Muenster, Germany
hschulen@uni-muenster.de
SO Zoology (Jena), (2002) Vol. 105, No. Supplement 5, pp. 28. print.
Meeting Info.: 95th Annual Meeting of the Deutsche Zoologische Gesellschaft (German Zoological Society). Halle/Saale, Germany. May 20-24, 2002.
ISSN: 0944-2006.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 7 Aug 2002
Last Updated on STN: 7 Aug 2002

L9 ANSWER 6 OF 19 MEDLINE on STN DUPLICATE 1
AN 2002334369 MEDLINE
DN PubMed ID: 12076767
TI A cathepsin L protease essential for Caenorhabditis elegans embryogenesis is functionally conserved in parasitic nematodes.
AU Britton Collette; Murray Linda
CS Wellcome Centre for Molecular Parasitology, University of Glasgow, Scotland, UK.. cb32n@udcf.gla.ac.uk
SO Molecular and biochemical parasitology, (2002 Jun) 122 (1) 21-33.
Journal code: 8006324. ISSN: 0166-6851.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF320084; GENBANK-AF412313; GENBANK-AY004155; GENBANK-AY039742; GENBANK-AY039743; GENBANK-AY057110; GENBANK-AY057111; GENBANK-AY069923
EM 200210
ED Entered STN: 20020623
Last Updated on STN: 20021008
Entered Medline: 20021004
AB Proteolytic enzymes are involved in processes important to development and survival of many organisms. Parasite proteases are considered potential targets of parasite control yet, for most, their precise physiological functions are unknown. Validation of potential targets requires analysis of function. We have recently identified a cathepsin L (CPL) cysteine protease, Ce-CPL-1, which is essential for embryonic development of the free-living nematode Caenorhabditis elegans. We now show that CPL genes closely related to Ce-cpl-1 are expressed in the animal parasitic nematodes Haemonchus contortus, Dictyocaulus viviparus, Teladorsagia circumcincta, Ancylostoma caninum and Ascaris suum, as well as in plant parasitic nematodes. The similarities in gene structure and encoded amino

acid sequence indicate that the **parasite** and **C. elegans** CPLs are homologous enzymes. We demonstrate functional compensation of the loss of C. elegans cpl-1 by transgenic expression of the H. contortus cpl-1 gene, rescuing the embryonic lethality. These genes may therefore be orthologues, sharing the same function in both species. Targeting of this enzyme has potential in inhibiting development and transmission of parasitic nematodes. In addition, the role of CPL is important to our understanding of nematode development.

L9 ANSWER 7 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:862827 CAPLUS
DN 138:181748
TI Conservation of long-range synteny and microsynteny between the genomes of two distantly related nematodes
AU Guiliano, D. B.; Hall, N.; Jones, S. J. M.; Clark, L. N.; Corton, C. H.; Barrell, B. G.; Blaxter, M. L.
CS Inst. of Cell, Animal and Population Biology, Univ. of Edinburgh, Edinburg, EH93JT, UK
SO GenomeBiology [online computer file] (2002), 3(10), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://www.genomebiology.com/content/pdf/gb-2002-3-10-research0057.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Comparisons between the genomes of the closely related nematodes Caenorhabditis elegans and Caenorhabditis briggsae reveal high rates of rearrangement, which a bias towards within-chromosome events. To assess whether this pattern is true of nematodes in general, we have used genome sequence to compare two nematode species that last shared a common ancestor approx. 300 million years ago: the model **C. elegans** and the filarial **parasite** Brugia malayi. An 83 kb region flanking the gene for Bm-mif-I (macrophage migration inhibitory factor, a B. malayi homolog of a human cytokine) was sequenced. When compared to the complete genome of C. elegans, evidence for conservation of long-range synteny and microsynteny was found. Potential C. elegans orthologs for 11 of the 12 protein-coding genes predicted in the B. malayi sequence were identified. Ten of these orthologs were located on chromosome I, with eight clustered in a 2.3 Mb region. While several, relatively local, intrachromosomal rearrangements have occurred, the order, composition, and configuration of two gene clusters, each containing three genes, was conserved. Comparison of B. malayi BAC-end genome survey sequence to C. elegans also revealed a bias towards intrachromosome rearrangements. In conclusion, we suggest that intrachromosomal rearrangement is a major force driving chromosomal organization in nematodes, but is constrained by the interdigitation of functional elements of neighboring genes.
RE.CNT 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 8 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:265844 BIOSIS
DN PREV200100265844
TI Characterization of a novel family of large ADP-ribosylation factor-specific guanine nucleotide exchange factors.
AU Lasell, Troy Kevin Robert [Reprint author]; Melancon, Paul [Reprint author]
CS University of Alberta, Medical Sciences Building, Room 5-35, Edmonton, Alberta, T6G-2H7, Canada
SO FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A1176. print.
Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology 2001. Orlando, Florida, USA. March 31-April 04, 2001.

CODEN: FAJOEC. ISSN: 0892-6638.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 6 Jun 2001
Last Updated on STN: 19 Feb 2002
AB Members of the ARF family of small GTPases play a vital role in regulating several effectors implicated in cargo selection and vesicle formation. All ARF-specific GEFs characterized to date contain a central Sec7 domain that was shown to be sufficient for activity. To date, three major families of ARF GEFs have been defined based on protein size, sequence similarity, presence of pleckstrin homology (PH) domain and sensitivity to the fungal metabolite brefeldin A (BFA). Here we report the identification in silico of a novel family of large (>170 kDa) and ubiquitously expressed sec7d ARF GEFs. There are three homologues in H. sapiens, with single orthologues in C. elegans and D. melanogaster, but none in S. cerevisiae or S. pombe. Available sequence data suggests these proteins, like GBF1 and BIG1/BIG2, lack PH domains. To confirm the GEF activity of this family, a series of sec7 domain chimaeras were generated. A relatively pure preparation of an active construct produced efficient GTP loading on both class I and class II ARFs at a 20:1 enzyme to substrate ratio. The sequence of motif 2 in the sec7 domain of all three human homologues begins with residues (ILAFAIILLNTDMY), suggesting BFA resistance (FA) rather than BFA sensitivity (YS). Further in vitro assays with recombinant enzyme confirmed this prediction. Detailed immunolocalization with antisera raised against recombinant protein will be presented.

L9 ANSWER 9 OF 19 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2001:376972 SCISEARCH
GA The Genuine Article (R) Number: 427RP
TI PCR amplification of putative gpa-2 and gpa-3 orthologs from the (A+T)-rich genome of Strongyloides stercoralis
AU Massey H C (Reprint); Ball C C; Lok J B
CS Univ Penn, Sch Vet Med, Dept Pathobiol, 3800 Spruce St, Philadelphia, PA 19104 USA (Reprint); Univ Penn, Sch Vet Med, Dept Pathobiol, Philadelphia, PA 19104 USA
CYA USA
SO INTERNATIONAL JOURNAL FOR PARASITOLOGY, (APR 2001) Vol. 31, No. 4, pp. 377-383.
Publisher: PERGAMON-ELSEVIER SCIENCE LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON, OXFORD OX5 1GB, ENGLAND.
ISSN: 0020-7519.
DT Article; Journal
LA English
REC Reference Count: 24
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Two G protein alpha subunit genes orthologous to gpa-2 and gpa-3 in Caenorhabditis elegans have been identified in the parasitic nematode. Strongyloides stercoralis. These genes mediate chemosensory signal transduction regulating dauer arrest in **C. elegans**. In the **parasite**. they represent candidate mediators for regulation of the choice between free-living and parasitic life cycles, the obligatory developmental arrest of infective larvae. and reactivation of development after infection. The (A + T) content of these genes is 72.2% for coding sequences. 90% for introns, and 84.1% for 5' and 3' flanking regions, requiring the use of low extension temperatures for long distance PCR. The possible significance of conserved structural motifs of these proteins is discussed. (C) 2001 Australian Society for Parasitology Inc. Published by Elsevier Science Ltd. All rights reserved.

L9 ANSWER 10 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:670726 CAPLUS
DN 135:316070

TI What can Caenorhabditis elegans tell us about nematocides and parasites?
AU Dent, Joseph A.
CS Department of Biology, McGill University, Montreal, QC, H3A1B1, Can.
SO Biotechnology and Bioprocess Engineering (2001), 6(4), 252-263
CODEN: BBEIAU; ISSN: 1226-8372
PB Korean Society for Biotechnology and Bioengineering
DT Journal; General Review
LA English
AB A review, with refs. Nematode infections compromise human health and reduce agricultural productivity. Expts. that exploit the powerful mol. genetics of the free-living nematode Caenorhabditis elegans have contributed to the authors' understanding of how the major classes of anthelmintic nematocides kill worms and how worms might evolve resistance to these drugs. In **C. elegans**, as in **parasites**, benzimidizoles interfere with microtubule polymerization, the imidazothiazoles/tetrahydropyrimidines activate nicotinic acetylcholine receptors, and the macrocyclic lactones activate glutamate-gated chloride channels. Mutant alleles of genes that encode drug targets often confer resistance in C. elegans. Preliminary evidence suggests that alleles of homologous genes in parasites will, in many cases, also play a role in resistance. Thus, information acquired from C. elegans can be usefully applied to understand the mechanisms of drug sensitivity and the genetics of resistance in parasites.
RE.CNT 108 THERE ARE 108 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 11 OF 19 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2001:925274 SCISEARCH
GA The Genuine Article (R) Number: 493JK
TI Gene structure of the extracellular glutathione S-transferase from Onchocerca volvulus and its overexpression and promoter analysis in transgenic Caenorhabditis elegans
AU Krause S; Sommer A; Fischer P; Brophy P M; Walter R D; Liebau E (Reprint)
CS Bernhard Nocht Inst Trop Med, Dept Biochem Parasitol, Bernhard Nocht Str 74, D-20359 Hamburg, Germany (Reprint); Bernhard Nocht Inst Trop Med, Dept Biochem Parasitol, D-20359 Hamburg, Germany; Bernhard Nocht Inst Trop Med, Sect Parasitol, D-20359 Hamburg, Germany; Univ Wales, Inst Biol Sci, Aberystwyth SY23 3DA, Dyfed, Wales
CYA Germany; Wales
SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (OCT 2001) Vol. 117, No. 2, pp. 145-154.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0166-6851.
DT Article; Journal
LA English
REC Reference Count: 37
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Two highly similar genes encoding unique extracellular, glycosylated glutathione S-transferases (GSTs) of the human-pathogenic nematode, Onchocerca volvulus (Ov-GST1a and Ov-GST1b), have been isolated and characterised, The genes are approximate to 3 kb in length and consist of seven exons interrupted by introns of approximate to 100 bp in length, with the exception of intron II, which is approximate to 1.6 kb in length. Interestingly, exon I and II encode a signal peptide and an N-terminal extension before sequence homology to other GSTs begins. The 5' flanking region was sequenced and analysed for transcription factor binding sites. Consistent with the lack of a TATA box. analysis of the mRNAs by primer extension showed multiple transcription start sites spread over a 60 bp region. To examine the activity and specificity of the Ov-GST1a gene promoter, we have exploited Caenorhabditis elegans as a heterologous transformation system. To analyse whether transgenic C. elegans are able to carry out processing and post-transcriptional modifications of the Ov-GST1a correctly. the protein was ectopically overexpressed in **C**

. **elegans**. The **parasite**-derived Ov-GST1a gene product was correctly processed in transgenic C. elegans and posttranslational modifications., such as signal peptide cleavage and N-glycosylation, were performed successfully. This further demonstrates the potential of C. elegans as a host for expression of candidate vaccine antigens from O. volvulus and affirms the role of C. elegans as a model for parasitic nematodes. (C) 2001 Elsevier Science B.V. All rights reserved.

L9 ANSWER 12 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:510706 BIOSIS
DN PREV199900510706
TI Caenorhabditis elegans as a biomonitor for immunological stress in nematodes.
AU Nowell, M. A.; De Pomerai, D. I.; Pritchard, D. I. [Reprint author]
CS School of Pharmaceutical Sciences, University of Nottingham, University Park, Nottingham, NG7 2RD, UK
SO Parasite Immunology (Oxford), (Oct., 1999) Vol. 21, No. 10, pp. 495-505. print.
CODEN: PAIMD8. ISSN: 0141-9838.
DT Article
LA English
ED Entered STN: 3 Dec 1999
Last Updated on STN: 3 Dec 1999
AB An experimental system has been developed using Caenorhabditis elegans (Secernentea: Rhabditida), to monitor immunological stress in nematodes. The transgenic C. elegans strain PC72 carries a lacZ reporter gene fused to a C. elegans hsp16-1 gene, which is inducible for beta-galactosidase activity at the heat stress temperature of 26degreeC. The investigate the possibility of using PC72 to monitor immunological stress, its surface coat was targeted, to mimic immune attack, by raising immune sera against surface coat components selectively removed by the cationic detergent cetyltrimethylammoniunm bromide. Initially, a highly significant induction of beta-galactosidase activity was seen in PC72 incubated in either surface-reactive or naive rabbit serum. Complement (C3) was detected over the entire surface of adult PC72 and was thought to be responsible for stress-induction with naive sera. When the immunoglobulin (Ig)G fraction of naive sera was used in isolation, no stress-induction was seen. In contrast, a two-fold increase in beta-galactosidase activity was seen in the presence of surface-reactive IgG (SR-IgG) which recognised surface components of between 6 and 40 kDa in western blot. The belief that surface reactive IgG could induce a stress response was reinforced by analysis of hsp-16 protein expression. Cationised ferritin was then used to assess whether stress-induction was truly a surface reactive event; binding of cationised ferritin to the nematode surface also resulted in two-fold induction of beta-galactosidase activity. To investigate the downstream biological effects of stress induction, worm growth and fecundity were measured in the presence of IgG preparations. A significant reduction was seen in both worm length and fecundity only when larvae were incubated in surface-reactive IgG, compared to both naive IgG and K-medium controls. In conclusion, it would appear that C. elegans is a suitable model to monitor the induction of immunological stress at the level of the nematode surface coat. Given the ability of nematode surface antigens to protect the vaccinated host in animal model systems, and the close phylogenetic relationships which exist between C. elegans and nematodes of medical and veterinary importance, it is conceivable that the immunological targets in or on the surface of C. elegans warrant rapid identification.

L9 ANSWER 13 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
AN 1999:721452 CAPLUS
DN 132:59664
TI The Caenorhabditis elegans genome: a guide in the post genomics age
AU Bird, David McK; Opperman, Charles H.; Jones, Steven J. M.; Baillie, David L.

CS Plant Nematode Genetics Group, Department of Plant Pathology, North Carolina State University, Raleigh, NC, 27695, USA
SO Annual Review of Phytopathology (1999), 37, 247-265
CODEN: APPYAG; ISSN: 0066-4286
PB Annual Reviews Inc.
DT Journal; General Review
LA English
AB A review with 67 refs. The completion of the entire genome sequence of the free-living nematode, Caenorhabditis elegans is a tremendous milestone in modern biol. Not only will scientists be poring over data mined from this resource, but techniques and methodologies developed along the way have changed the way the authors can approach biol. questions. The completion of the C. elegans genomic sequence will be of particular importance to scientists working on parasitic nematodes. In many cases, these nematode species present intractable challenges to those interested in their biol. and genetics. The data already compared from **parasites** to the **C. elegans** database reveals a wealth of opportunities for parasite biologists. It is likely that many of the same genes will be present in parasites and that these genes will have similar functions. Addnl. information regarding differences between free-living and parasitic species will provide insight into the evolution and nature of parasitism. Finally, genetic and genomic approaches to the study of parasitic nematodes now have a clearly marked path to follow.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 14 OF 19 MEDLINE on STN DUPLICATE 3
AN 2000017523 MEDLINE
DN PubMed ID: 10551361
TI Identification of promoter elements of parasite nematode genes in transgenic Caenorhabditis elegans.
AU Britton C; Redmond D L; Knox D P; McKerrow J H; Barry J D
CS Wellcome Centre for Molecular Parasitology, University of Glasgow, Scotland, UK.. cb32n@udcf.gla.ac.uk
NC AI 20452 (NIAID)
SO Molecular and biochemical parasitology, (1999 Oct 15) 103 (2) 171-81.
Journal code: 8006324. ISSN: 0166-6851.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF079402; GENBANK-AF116182; GENBANK-X96731
EM 199912
ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991223
AB Transformation of the free-living nematode Caenorhabditis elegans with promoter/reporter gene constructs is a very powerful technique to examine and dissect gene regulatory mechanisms. No such transformation system is available for parasitic nematode species. We have exploited C. elegans as a heterologous transformation system to examine activity and specificity of parasitic nematode gene promoters. Using three different parasite promoter/lac Z reporter constructs strict tissue-specific expression is observed. Upstream sequences of the Haemonchus contortus gut pepsinogen gene pep-1 and cysteine protease gene AC-2 direct expression exclusively in gut cells, while promoter sequence of the Ostertagia circumcincta cuticular collagen gene colost-1 directs hypodermal-specific expression. Mutation analysis indicates that AC-2 promoter function is dependent on a GATA-like motif close to the translation start site, similar to our findings with the C. elegans cpr-1 cysteine protease gene. While the spatial expression of these **parasite** promoters in **C. elegans** correlates with their expression in the **parasite**, the exact timing of expression does not. This suggests that regulatory mechanisms influencing the timing of expression may have evolved more

rapidly than those controlling spatial expression of structural genes.

L9 ANSWER 15 OF 19 MEDLINE on STN DUPLICATE 4
AN 1999069618 MEDLINE
DN PubMed ID: 9851921
TI Caenorhabditis elegans is a nematode.
AU Blaxter M
CS Institute of Cell, Animal, and Population Biology, University of Edinburgh, Edinburgh EH9 3JT, UK.
SO Science, (1998 Dec 11) 282 (5396) 2041-6. Ref: 45
Journal code: 0404511. ISSN: 0036-8075.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199812
ED Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981224
AB Caenorhabditis elegans is a rhabditid nematode. What relevance does this have for the interpretation of the complete genome sequence, and how will it affect the exploitation of the sequence for scientific and social ends? Nematodes are only distantly related to humans and other animal groups; will this limit the universality of the **C. elegans** story? Many nematodes are **parasites**; can knowledge of the **C. elegans** sequence aid in the prevention and treatment of disease?

L9 ANSWER 16 OF 19 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 5
AN 1998:163842 BIOSIS
DN PREV199800163842
TI Temperature effects on efficacy of Choetospila elegans (Hymenoptera: Pteromalidae) to suppress Rhyzopertha dominica (Coleoptera: Bostrichidae) in stored wheat.
AU Flinn, P. W. [Reprint author]
CS Grain Marketing Production Res. Cent., USDA-ARS, Manhattan, KS 66502, USA
SO Journal of Economic Entomology, (Feb., 1998) Vol. 91, No. 1, pp. 320-323. print.
CODEN: JEENAI. ISSN: 0022-0493.
DT Article
LA English
ED Entered STN: 6 Apr 1998
Last Updated on STN: 6 Apr 1998
AB Laboratory studies were conducted to assess the effectiveness of the parasitoid wasp Choetospila elegans (Westwood) for controlling Rhyzopertha dominica (F.), lesser grain borer, in wheat at 32 and 25degreeC. The 2 temperature regimes were used to simulate an unaerated bin of wheat and a bin aerated at harvest time. Two adult male and 2 adult female R. dominica were each released into containers with 19 kg of hard red winter wheat. An equal number of adult C. elegans were released into half of the containers. Half the containers were kept at 25degreeC and half at 32degreeC. Suppression of R. dominica population growth by C. elegans was much greater at 25 than at 32degreeC. After 161 d, R. dominica density in the containers with C. elegans was 9,185/kg at 32degreeC, and 10/kg at 25degreeC. At 25ETA, C. elegans was able to locate and parasitize most of the larvae that were produced by the adult beetles. This resulted in a very high level of population suppression (99% in comparison to the control at 25degreeC). In contrast, at 32degreeC, beetle suppression was only 50% in comparison to containers without C. elegans at this temperature. This study suggests that when augmentative **parasite** releases are made with **C. elegans**, better host

suppression would be achieved by cooling the grain to 25degreeC shortly after harvest, rather than leaving it unaerated for the summer.

L9 ANSWER 17 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:715865 CAPLUS
DN 130:78816
TI Caenorhabditis elegans: a genetic guide to parasitic nematode biology
AU Bird, D. McK.; Opperman, C. H.
CS Department of Plant Pathology, North Carolina State University, Raleigh, NC, 27695-7616, USA
SO Journal of Nematology (1998), 30(3), 299-308
CODEN: JONEB5; ISSN: 0022-300X
PB Society of Nematologists
DT Journal; General Review
LA English
AB A review, with 37 refs. The advent of parasite genome sequencing projects, as well as an increase in biol.-directed gene discovery, promises to reveal genes encoding many of the key mols. required for nematode-host interactions. However, distinguishing parasitism genes from those merely required for nematode viability remains a substantial challenge. Although this will ultimately require a functional test in the host or **parasite**, the free-living nematode **C. elegans** can be exploited as a heterologous system to determine function of candidate parasitism genes. Studies of C. elegans also have revealed genetic networks, such as the dauer pathway, that may also be important adaptations for parasitism. As a more directed means of identifying parasitism traits, we developed classical genetics for Heterodera glycines and have used this approach to map genes conferring host resistance-breaking phenotypes. It is likely that the C. elegans and H. glycines genomes will be at least partially syntenic, thus permitting predictive phys. mapping of H. glycines genes of interest.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 18 OF 19 MEDLINE on STN DUPLICATE 6
AN 95182458 MEDLINE
DN PubMed ID: 7877171
TI Beta-tubulin genes from the parasitic nematode Haemonchus contortus modulate drug resistance in Caenorhabditis elegans.
AU Kwa M S; Veenstra J G; Van Dijk M; Roos M H
CS Department of Parasitology and Tropical Veterinary Medicine, Faculty of Veterinary Medicine, University of Utrecht, The Netherlands.
SO Journal of molecular biology, (1995 Mar 3) 246 (4) 500-10.
Journal code: 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X67488; GENBANK-X80046; GENBANK-X80047; GENBANK-X80048; GENBANK-X80049
EM 199504
ED Entered STN: 19950419
Last Updated on STN: 19950419
Entered Medline: 19950405
AB Resistance to antimitotic chemotherapeutics in pathogenic nematodes, fungi and mammalian cells is closely associated with structural changes in cytoskeletal beta-tubulin. We investigated the possibility of using the well-characterised free-living nematode Caenorhabditis elegans as a model for studying the mechanism of resistance against benzimidazole (BZ) drugs in the parasitic nematode Haemonchus contortus. Functional analysis of a conserved beta-tubulin isotype (tub-1) mutation near GTP-binding domain II, which is linked to BZ resistance, was carried out in **C. elegans** by heterologous expression of: (1) **parasite** BZ-sensitive alleles; (2) BZ-resistant alleles; and (3) in vitro

mutagenised beta-tubulin gene constructs. The injected heterologous gene constructs were not only stably maintained, but also expressed as shown by reverse transcriptase-polymerase chain reaction analysis. The degree of BZ drug susceptibility of the transformants was assayed and quantified by incubation with both benomyl and thiabendazol. All H. contortus tub-1 constructs, which encoded Phe at position 200, conferred susceptibility to thiabendazole in BZ-resistant C. elegans ben-1 mutants. In contrast, constructs carrying Tyr200 did not alter the BZ drug phenotype. From these experiments we conclude that: (1) C. elegans can be used as an expression host, since injected parasite genes were biologically active; and (2) the single Phe to Tyr mutation at position 200 in beta-tubulin isotype 1 is the cause of BZ resistance in H. contortus.

L9 ANSWER 19 OF 19 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 95:517973 SCISEARCH
GA The Genuine Article (R) Number: RL259
TI IMMUNO-GOLD-LABELING OF CUT-1, CUT-2 AND CUTICLIN EPITOPES IN CAENORHABDITIS-ELEGANS AND HETERORHABDITIS SP PROCESSED BY HIGH-PRESSURE FREEZING AND FREEZE-SUBSTITUTION
AU FAVRE R (Reprint); HERMANN R; CERMOLA M; HOHENBERG H; MULLER M; BAZZICALUPO P
CS CNR, IST INT GENET & BIOFIS, VIA GUGLIELMO MARCONI 10, I-80125 NAPLES, ITALY (Reprint); SWISS FED INST TECHNOL, ZURICH, SWITZERLAND; HEINRICH PETTE INST, HAMBURG, GERMANY
CYA ITALY; SWITZERLAND; GERMANY
SO JOURNAL OF SUBMICROSCOPIC CYTOLOGY AND PATHOLOGY, (JUL 1995) Vol. 27, No. 3, pp. 341-347.
ISSN: 1122-9497.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 15
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB CUT-1 and CUT-2 are two distinct protein components of cuticlin, the insoluble residue of the cuticles of nematodes. In previous experiments of gold-immuno-labelling on sections of chemically fixed Caenorbabditis elegans, CUT-1 and CUT-2 epitopes were specifically lost. Cryo-immobilization of C. elegans under high pressure followed by freeze-substitution, however, resulted in a good preservation of these antigenic sites and of the ultrastructure of the worms. The entomopathogenic nematode Heterorhabditis sp. processed by the same cryopreparation protocol has shown a strong reactivity with anti-sera raised against CUT-1, CUT-2 and against the whole cuticlin residue of C. elegans. The localization of these epitopes was conserved across the two species.

=> d his

(FILE 'HOME' ENTERED AT 18:29:31 ON 24 MAR 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 18:29:44 ON 24 MAR 2004

L1 20381 S C(W)ELEGANS
L2 26952 S SENSITIVE(5A)(DRUG OR AGENT OR CHEMICALS)
L3 0 S L1(7A)L2
L4 18 S L1 AND L2
L5 434 S L1 AND PARASITE
L6 0 S L5 AND L2
L7 5 DUP REM L4 (13 DUPLICATES REMOVED)
L8 33 S L1(6A)PARASITE
L9 19 DUP REM L8 (14 DUPLICATES REMOVED)

=>